Resource Summary Report

Generated by NIF on Apr 8, 2025

Pegasus

RRID:SCR_021645
Type: Tool

Proper Citation

Pegasus (RRID:SCR_021645)

Resource Information

URL: https://pegasus.readthedocs.io/en/stable

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Description: Software package for massive single cell data processing. Enables analysis of million scale single cell RNA-seq data and is functionally comparable to Seurat and SCANPY. Command line tool, Python package and base for Cloud based analysis workflows. Supports variety of analysis tasks, such as cell and gene level quality control, highly variable gene selection, dimension reduction, kNN graph building, data integration, clustering, differential expression analysis and putative cell type annotation.

Synonyms: Pegasus for Single Cell Analysis, Pegasus tool for massive single cell data processing

Resource Type: software application, software toolkit, data analysis software, data processing software, software resource

Keywords: massive single cell data processing, million scale single cell RNA-seq data, gene level quality control, highly variable gene selection, dimension reduction

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Pegasus

Resource ID: SCR_021645

Alternate URLs: https://app.terra.bio/#workspaces/kco-tech/Cumulus/notebooks

Record Creation Time: 20220129T080356+0000

Record Last Update: 20250407T220623+0000

Ratings and Alerts

No rating or validation information has been found for Pegasus.

No alerts have been found for Pegasus.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 29 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zhang Z, et al. (2025) Brain-model neural similarity reveals abstractive summarization performance. Scientific reports, 15(1), 370.

Xu S, et al. (2024) scACT: Accurate Cross-modality Translation via Cycle-consistent Training from Unpaired Single-cell Data. Proceedings of the ... ACM International Conference on Information & Knowledge Management. ACM International Conference on Information and Knowledge Management, 2024, 2722.

Dorrell RG, et al. (2024) Complementary environmental analysis and functional characterization of lower glycolysis-gluconeogenesis in the diatom plastid. The Plant cell, 36(9), 3584.

Kehl MS, et al. (2024) Single-neuron representations of odours in the human brain. Nature, 634(8034), 626.

Mulherin BP, et al. (2024) Normalization of Hemoglobin, Lactate Dehydrogenase, and Fatigue in Patients with Paroxysmal Nocturnal Hemoglobinuria Treated with Pegcetacoplan. Drugs in R&D, 24(2), 169.

Gerayeli FV, et al. (2024) Single-cell sequencing reveals cellular landscape alterations in the airway mucosa of patients with pulmonary long COVID. The European respiratory journal, 64(5).

Oh DS, et al. (2024) SARS-CoV-2 infection elucidates features of pregnancy-specific immunity. Cell reports, 43(11), 114933.

Gao X, et al. (2024) Pre-training with a rational approach for antibody sequence representation. Frontiers in immunology, 15, 1468599.

N M P, et al. (2024) A multi-region single nucleus transcriptomic atlas of Parkinson's disease. Scientific data, 11(1), 1274.

Jia R, et al. (2024) Immunological characterization and comparison of children with COVID-19 from their adult counterparts at single-cell resolution. Frontiers in immunology, 15, 1358725.

Wang K, et al. (2024) UniFORM: Towards Universal Immunofluorescence Normalization for Multiplex Tissue Imaging. bioRxiv : the preprint server for biology.

Visonà G, et al. (2024) Network propagation for GWAS analysis: a practical guide to leveraging molecular networks for disease gene discovery. Briefings in bioinformatics, 25(2).

De Zuani M, et al. (2024) Single-cell and spatial transcriptomics analysis of non-small cell lung cancer. Nature communications, 15(1), 4388.

Volkov DL, et al. (2024) Florida Current transport observations reveal four decades of steady state. Nature communications, 15(1), 7780.

Pisu D, et al. (2024) The frequency of CD38+ alveolar macrophages correlates with early control of M. tuberculosis in the murine lung. Nature communications, 15(1), 8522.

Yang R, et al. (2024) Ascle-A Python Natural Language Processing Toolkit for Medical Text Generation: Development and Evaluation Study. Journal of medical Internet research, 26, e60601.

Russell D, et al. (2024) CD38+ Alveolar macrophages mediate early control of M. tuberculosis proliferation in the lung. Research square.

Zeng B, et al. (2024) Single-Nucleus Atlas of Cell-Type Specific Genetic Regulation in the Human Brain. Research square.

Duan Z, et al. (2023) iHerd: an integrative hierarchical graph representation learning framework to quantify network changes and prioritize risk genes in disease. PLoS computational biology, 19(9), e1011444.

Duffy MF, et al. (2023) Divergent patterns of healthy aging across human brain regions at single-cell resolution reveal links to neurodegenerative disease. bioRxiv : the preprint server for biology.